GenCore version 5.1.3


OM nucleic - nucleic search, using sw model

Run on: October 23, 2002, 06:19:54 ; Search time 983.832 Seconds
(without alignments)
1169.874 Million cell updates/sec

Title: US-09-938-013A-2
Perfect score: 55
Sequence: 1 gaaatgctggcatagagcag.....ctaaagaaacgatcagacag 55

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 55 | 100.0 | 1266 | 9 | HSSMNEUR8 | U43883 Human survi |
| 2 | 55 | 100.0 | 1408 | 6 | A77034 | A77034 Sequence 11 |
| 3 | 55 | 100.0 | 1408 | 6 | A77036 | A77036 Sequence 13 |
| 4 | 55 | 100.0 | 1408 | 6 | AR100219 | AR100219 Sequence |
| 5 | 55 | 100.0 | 1408 | 6 | AR100221 | AR100221 Sequence |
| 6 | 55 | 100.0 | 1442 | 9 | BC000908 | BC000908 Homo sapi |
| 7 | 55 | 100.0 | 1466 | 9 | HSU21914 | U21914 Human dupli |
| 8 | 55 | 100.0 | 1491 | 9 | HSU18423 | U18423 Human spina |
| 9 | 55 | 100.0 | 1525 | 9 | BC015308 | BC015308 Homo sapi |
| 10 | 55 | 100.0 | 1582 | 6 | A77033 | A77033 Sequence 10 |
| 11 | 55 | 100.0 | 1582 | 6 | A77035 | A77035 Sequence 12 |
| 12 | 55 | 100.0 | 1582 | 6 | AR100218 | AR100218 Sequence |
| 13 | 55 | 100.0 | 1582 | 6 | AR100220 | AR100220 Sequence |
| 14 | 55 | 100.0 | 3271 | 6 | AR100228 | AR100228 Sequence |
| c 15 | 55 | 100.0 | 82976 | 9 | AC005031 | AC005031 Homo sapi |
| 16 | 55 | 100.0 | 113213 | 9 | AC016554 | AC016554 Homo sapi |
| c 17 | 55 | 100.0 | 129541 | 9 | AC004999 | AC004999 Homo sapi |
| c 18 | 55 | 100.0 | 131078 | 9 | HSU80017 | U80017 Homo sapien |
| 19 | 55 | 100.0 | 155306 | 2 | AC010272 | AC010272 Homo sapi |
| 20 | 55 | 100.0 | 155974 | 9 | AC022119 | AC022119 Homo sapi |
| c 21 | 55 | 100.0 | 168814 | 9 | AC010237 | AC010237 Homo sapi |
| 22 | 55 | 100.0 | 190871 | 9 | AC044797 | AC044797 Homo sapi |
| 23 | 46 | 83.6 | 885 | 6 | AR022360 | AR022360 Sequence |
| 24 | 32 | 58.2 | 1643 | 9 | HSU91640 | U91640 Human survi |
| 25 | 32 | 58.2 | 42210 | 9 | AC002050 | AC002050 Homo sapi |
| 26 | 32 | 58.2 | 155780 | 9 | HS336O12 | AL513498 Homo sapi |
| 27 | 32 | 58.2 | 175695 | 2 | AL606844 | AL606844 Homo sapi |
| 28 | 32 | 58.2 | 178631 | 9 | AL512635 | AL512635 Human DNA |
| 29 | 30 | 54.5 | 206074 | 9 | AC009484 | AC009484 Homo sapi |
| 30 | 28 | 50.9 | 113735 | 2 | AC091881 | AC091881 Homo sapi |
| c 31 | 28 | 50.9 | 138841 | 2 | AC092354 | AC092354 Homo sapi |
| c 32 | 28 | 50.9 | 156486 | 2 | AC011657 | AC011657 Homo sapi |
| 33 | 28 | 50.9 | 163384 | 9 | AC009180 | AC009180 Homo sapi |
| c 34 | 27.4 | 49.8 | 154157 | 9 | HS101D08 | AL133492 Homo sapi |
| c 35 | 27.4 | 49.8 | 340000 | 9 | HS21C103 | AL163303 Homo sapi |
| 36 | 27.2 | 49.5 | 164988 | 2 | AC080070 | AC080070 Homo sapi |
| c 37 | 27.2 | 49.5 | 177720 | 9 | AC019193 | AC019193 Homo sapi |
| c 38 | 27 | 49.1 | 149546 | 9 | AC087256 | AC087256 Homo sapi |
| 39 | 27 | 49.1 | 152167 | 2 | AC073307 | AC073307 Homo sapi |
| 40 | 27 | 49.1 | 168227 | 9 | AC021868 | AC021868 Homo sapi |
| c 41 | 27 | 49.1 | 173239 | 9 | AC006478 | AC006478 Homo sapi |
| c 42 | 27 | 49.1 | 196817 | 9 | AC019209 | AC019209 Homo sapi |
| c 43 | 26.8 | 48.7 | 259487 | 10 | AL365322 | AL365322 Mouse DNA |
| c 44 | 26.2 | 47.6 | 111949 | 2 | AL353755 | AL353755 Homo sapi |
| 45 | 26.2 | 47.6 | 212854 | 2 | AC093028 | AC093028 Homo sapi |

ALIGNMENTS

RESULT 1
HSSMNEUR8
LOCUS HSSMNEUR8 1266 bp DNA linear PRI 16-MAY-1996
DEFINITION Human survival motor neuron (SMN) gene, exons 7 and 8, and complete cds.
ACCESSION U43883
VERSION U43883.1 GI:1314344
KEYWORDS spinal muscular atrophy gene.
SEGMENT 8 of 8
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1266)
AUTHORS Lefebvre,S., Burglen,L., Reboullet,S., Clermont,O., Burlet,P., Viollet,L., Benichou,B., Cruaud,C., Millasseau,P., Zeviani,M. et al.
TITLE Identification and characterization of a spinal muscular atrophy-determining gene
JOURNAL Cell 80 (1), 155-165 (1995)
MEDLINE 95112343
REFERENCE 2 (bases 1 to 1266)
AUTHORS Burglen,L., Lefebvre,S., Clermont,O., Burlet,P., Viollet,L.,

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            Cruaud,C., Munnich,A. and Melki,J.
  TITLE     Structure and organization of the human survival motor neurone
            (SMN) gene
  JOURNAL   Genomics 32 (3), 479-482 (1996)
  MEDLINE   96435930
REFERENCE   3  (bases 1 to 1266)
  AUTHORS   Burglen,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-DEC-1995) Lydie Burglen, INSERM U-393, IFREM, Hopital
            Necker-Enfants Malades, 149, rue de Sevres Cedex 15, Paris 75743,
            France
COMMENT     Duplicated gene within the 5q13 region; interspecies conserved
            sequences. The SMN gene is present in two copies within the SMA
            (spinal muscular atrophy) candidate region on chromosome 5q13. The
            two copies are transcribed and are distinguished by sequence
            differences specific to the centromeric copy.
FEATURES             Location/Qualifiers
     source          1. .1266
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                     /db_xref="taxon:9606"
                     /chromosome="5"
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                     U43881.1:103. .198,U43882.1:53. .163,209. .262,707. .>1266)
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                     /note="spinal muscular atrophy gene; cDNA sequence found
                     in GenBank Accession Number U18423"
                     /product="survival motor neuron"
     gene            join(U43876.1:575. .762,U43877.1:1. .257,U43878.1:1. .314,
                     U43879.1:1. .357,U43880.1:1. .302,U43881.1:1. .251,
                     U43882.1:1. .244,1. .1266)
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     CDS             join(U43876.1:608. .688,U43877.1:104. .175,
                     U43878.1:118. .237,U43879.1:84. .284,U43880.1:69. .221,
                     U43881.1:103. .198,U43882.1:53. .163,209. .259)
                     /gene="SMN"
                     /note="spinal muscular atrophy gene"
                     /codon_start=1
                     /product="survival motor neuron"
                     /protein_id="AAC50473.1"
                     /db_xref="GI:1314346"
                     /translation="MAMSSGGSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYD
                     KAVASFKHALKNGDICETSGKPKTTPKRKPAKKNKSQKKNTAASLQQWKVGDKCSAIW
                     SEDGCIYPATIASIDFKRETCVVVYTGYGNREEQNLSDLLSPICEVANNIEQNAQENE
                     NESQVSTDESENSRSPGNKSDNIKPKSAPWNSFLPPPPPMPGPRLGPGKPGLKFNGPP
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     intron          <1. .208
                     /gene="SMN"
                     /number=6
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                     /note="a nucleotide change specific to the centromeric
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                     /citation=[1]
                     /replace="a"
     exon            209. .262
                     /gene="SMN"
                     /number=7
     misc_difference 214
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     3'UTR           join(260. .262,707. .>1266)
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     intron          263. .706
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                     /number=7
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                     /replace="g"
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                     /citation=[1]
                     /replace="g"
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                     /number=8
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  Best Local Similarity  100.0%;  Pred. No. 7.1e-09;
  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GAAATGCTGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGATCAGACAG 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    707 GAAATGCTGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGATCAGACAG 761


RESULT 2
A77034
LOCUS       A77034                 1408 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 11 from Patent EP0708178.
ACCESSION   A77034
VERSION     A77034.1  GI:6088824
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1408)
  AUTHORS   Melki,J. and Munnich,A.
  TITLE     SURVIVAL MOTOR NEURON (SMN) GENE: A GENE FOR SPINAL MUSCULAR
            ATROPHY
  JOURNAL   Patent: EP 0708178-A 11 24-APR-1996;
            INST NAT SANTE RECH MED (FR)
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     source          1. .1408
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      464 a    198 c    277 g    469 t
ORIGIN

  Query Match           100.0%;  Score 55;  DB 6;  Length 1408;
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  Matches   55;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GAAATGCTGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGATCAGACAG 55
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 GAAATGCTGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGATCAGACAG 900


RESULT 3
A77036
LOCUS       A77036                 1408 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 13 from Patent EP0708178.
ACCESSION   A77036
VERSION     A77036.1  GI:6088826
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1408)
  AUTHORS   Melki,J. and Munnich,A.
  TITLE     SURVIVAL MOTOR NEURON (SMN) GENE: A GENE FOR SPINAL MUSCULAR
            ATROPHY
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